

Invited speaker presentation

Emergence of novel retroviruses

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As with many viruses, retroviruses do not always restrict themselves to a single host species. Phylogenetic analyses of human and other primate retroviruses conducted during the past twenty years has revealed that the pandemic human retroviruses, human immunodeficiency viruses (HIV) and human T-lymphotropic viruses (HTLV), were each the result of multiple independent introductions of viruses from nonhuman primates (NHPs) to humans. Nevertheless, whether such transmission of retroviruses was limited to rare historical occurrences or is part of an ongoing process has remained unclear. A series of recent findings by our group, focused on occupationally exposed individuals, has demonstrated that far from being a historical oddity, the transmission of retroviruses from NHPs to humans is a regular and ongoing phenomenon. Here, we review the evidence for emerging retrovirus zoonosis, both from captive animals to lab workers and primate handlers, as well as from wild NHPs to people exposed through hunting, butchering, and keeping of wild animal 'pets' in central Africa. The results show that three new retroviruses previously undocumented in humans including the simian foamy viruses, HTLV-3, and HTLV-4 have all been identified in persons exposed to the blood and body fluids of NHPs. The regular transmission of primate retroviruses suggests that zoonosis, *per se*, may not be the rate limiting step in pandemic retrovirus emergence, and that other factors such as viral adaptation probably play an important role in successful cross-species transmission and pandemic human retrovirus emergence. The results reinforce the need for defining the public health implications of the emergence of the new retroviruses and for ongoing surveillance efforts aimed at documenting and predicting the retrovirus emergence process.